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Application Serial Number: 10/517,310
Source: PCT
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PATENT APPLICATION: US/10/517,310

DATE: 10/25/2005
TIME: 12:04:15

Input Set : A:\262507US0PCT.txt
Output Set: N:\CRF4\10252005\J517310.raw

3 <110> APPLICANT: KOTANI, HIDEHITO
4 MIZUARAI, SHINJI
6 <120> TITLE OF INVENTION: METHOD FOR PREDICTING A DRUG TRANSPORT CAPABILITY BY ABCG2
7 POLYMORPHISMS
9 <130> FILE REFERENCE: 262507US0PCT
11 <140> CURRENT APPLICATION NUMBER: 10/517,310
12 <141> CURRENT FILING DATE: 2004-12-17
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/07534
15 <151> PRIOR FILING DATE: 2003-06-13
17 <150> PRIOR APPLICATION NUMBER: JP 2002-175806
18 <151> PRIOR FILING DATE: 2002-06-17
20 <160> NUMBER OF SEQ ID NOS: 68
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1968
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1965)
34 <400> SEQUENCE: 1
35 atg tct tcc agt aat gtc gaa gtt ttt atc cca gtg tca caa gga aac 48
36 Met Ser Ser Ser Asn Val Glu Val Phe Ile Pro Val Ser Gln Gly Asn
37 1 5 10 15
39 acc aat ggc ttc ccc gcg aca gct tcc aat gac ctg aag gca ttt act 96
40 Thr Asn Gly Phe Pro Ala Thr Ala Ser Asn Asp Leu Lys Ala Phe Thr
41 20 25 30
43 gaa gga gct gtg tta agt ttt cat aac atc tgc tat cga gta aaa ctg 144
44 Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
45 35 40 45
47 aag agt ggc ttt cta cct tgt cga aaa cca gtt gag aaa gaa ata tta 192
48 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
49 50 55 60
51 tcg aat atc aat ggg atc atg aat cct ggt ctc aac gcc atc ctg gga 240
52 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
53 65 70 75 80
55 ccc aca ggt gga ggc aaa tct tcg tta tta gat gtc tta gct gca agg 288
56 Pro Thr Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
57 85 90 95
59 aaa gat cca agt gga tta tct gga gat gtt ctg ata aat gga gca ccg 336
60 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
61 100 105 110
63 cga cct gcc aat ttc aaa tgt aat tca ggt tac gtg gta caa gat gat 384

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64	Arg	Pro	Ala	Asn	Phe	Lys	Cys	Asn	Ser	Gly	Tyr	Val	Val	Gln	Asp	Asp	
65		115				120							125				
67	gtt	gtg	atg	ggc	act	ctg	acg	gtg	aga	gaa	aac	tta	cag	ttc	tca	gca	432
68	Val	Val	Met	Gly	Thr	Leu	Thr	Val	Arg	Glu	Asn	Leu	Gln	Phe	Ser	Ala	
69		130				135							140				
71	gct	ctt	cg	ttt	gca	aca	act	atg	acg	aat	cat	gaa	aaa	aac	gaa	cg	480
72	Ala	Leu	Arg	Leu	Ala	Thr	Thr	Met	Thr	Asn	His	Glu	Lys	Asn	Glu	Arg	
73	145					150					155			160			
75	att	aac	agg	gtc	att	caa	gag	tta	gg	tgt	ctg	gat	aaa	gtg	gca	gac	528
76	Ile	Asn	Arg	Val	Ile	Gln	Glu	Leu	Gly	Leu	Asp	Lys	Val	Ala	Asp	Ser	
77		165				170					175						
79	aag	gtt	gga	act	cag	ttt	atc	cgt	gg	tgt	tct	gga	gga	gaa	aga	aaa	576
80	Lys	Val	Gly	Thr	Gln	Phe	Ile	Arg	Gly	Val	Ser	Gly	Gly	Glu	Arg	Lys	
81		180				185					190						
83	agg	act	agt	ata	gga	atg	gag	ctt	atc	act	gat	cct	tcc	atc	ttg	ttc	624
84	Arg	Thr	Ser	Ile	Gly	Met	Glu	Leu	Ile	Thr	Asp	Pro	Ser	Ile	Leu	Phe	
85		195				200					205						
87	ttg	gat	gag	cct	aca	act	ggc	tta	gac	tca	agc	aca	gca	aat	gct	gtc	672
88	Leu	Asp	Glu	Pro	Thr	Thr	Gly	Leu	Asp	Ser	Ser	Thr	Ala	Asn	Ala	Val	
89	210					215					220						
91	ctt	ttg	ctc	ctg	aaa	agg	atg	tct	aag	cag	gga	cga	aca	atc	atc	tcc	720
92	Leu	Leu	Leu	Lys	Arg	Met	Ser	Lys	Gln	Gly	Arg	Thr	Ile	Ile	Phe		
93	225					230					235			240			
95	tcc	att	cat	cag	cct	cga	tat	tcc	atc	tcc	aag	ttg	ttt	gat	agc	ctc	768
96	Ser	Ile	His	Gln	Pro	Arg	Tyr	Ser	Ile	Phe	Lys	Leu	Phe	Asp	Ser	Leu	
97		245				250					255						
99	acc	tta	ttg	gcc	tca	gga	aga	ctt	atg	ttc	cac	ggg	cct	gct	cag	gag	816
100	Thr	Leu	Leu	Ala	Ser	Gly	Arg	Leu	Met	Phe	His	Gly	Pro	Ala	Gln	Glu	
101		260				265					270						
103	gcc	ttg	gga	tac	ttt	gaa	tca	gct	gg	tat	cac	tgt	gag	gcc	tat	aat	864
104	Ala	Leu	Gly	Tyr	Phe	Glu	Ser	Ala	Gly	Tyr	His	Cys	Glu	Ala	Tyr	Asn	
105		275				280					285						
107	aac	cct	gca	gac	ttc	ttc	ttg	gac	atc	att	aat	gga	gat	tcc	act	gct	912
108	Asn	Pro	Ala	Asp	Phe	Phe	Leu	Asp	Ile	Ile	Asn	Gly	Asp	Ser	Thr	Ala	
109		290				295					300						
111	gtt	gca	tta	aaa	aga	gaa	gac	ttt	aaa	gcc	aca	gag	atc	ata	gag		960
112	Val	Ala	Leu	Asn	Arg	Glu	Glu	Asp	Phe	Lys	Ala	Thr	Glu	Ile	Ile	Glu	
113	305					310					315			320			
115	cct	tcc	aag	cag	gat	aag	cca	ctc	ata	gaa	aaa	tta	gcg	gag	att	tat	1008
116	Pro	Ser	Lys	Gln	Asp	Lys	Pro	Leu	Ile	Glu	Lys	Leu	Ala	Glu	Ile	Tyr	
117		325				330					335						
119	gtc	aac	tcc	tcc	ttc	tac	aaa	gag	aca	aaa	gct	gaa	tta	cat	caa	ctt	1056
120	Val	Asn	Ser	Ser	Phe	Tyr	Lys	Glu	Thr	Lys	Ala	Glu	Leu	His	Gln	Leu	
121		340				345					350						
123	tcc	ggg	ggt	gag	aag	aag	aag	atc	aca	gtc	ttc	aag	gag	atc	agc		1104
124	Ser	Gly	Gly	Glu	Lys	Lys	Lys	Lys	Ile	Thr	Val	Phe	Lys	Glu	Ile	Ser	
125		355				360					365						
127	tac	acc	acc	tcc	ttc	tac	caa	ctc	aga	tgg	gtt	tcc	aag	cgt	tca		1152
128	Tyr	Thr	Thr	Ser	Phe	Cys	His	Gln	Leu	Arg	Trp	Val	Ser	Lys	Arg	Ser	

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129	370	375	380		
131	ttc aaa aac ttg ctg ggt aat ccc cag gcc tct ata gct cag atc att			1200	
132	Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile				
133	385	390	395	400	
135	gtc aca gtc gta ctg gga ctg gtt ata ggt gcc att tac ttt ggg cta			1248	
136	Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu				
137	405	410	415		
139	aaa aat gat tct act gga atc cag aac aga gct ggg gtt ctc ttc ttc			1296	
140	Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe				
141	420	425	430		
143	ctg acg acc aac cag tgt ttc agc agt gtt tca gcc gtg gaa ctc ttt			1344	
144	Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe				
145	435	440	445		
147	gtg gta gag aag aag ctc ttc ata cat gaa tac atc agc gga tac tac			1392	
148	Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr				
149	450	455	460		
151	aga gtg tca tct tat ttc ctt gga aaa ctg tta tct gat tta tta ccc			1440	
152	Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro				
153	465	470	475	480	
155	atg agg atg tta cca agt att ata ttt acc tgt ata gtg tac ttc atg			1488	
156	Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met				
157	485	490	495		
159	tta gga ttg aag cca aag gca gat gcc ttc ttc gtt atg atg ttt acc			1536	
160	Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr				
161	500	505	510		
163	ctt atg atg gtg gct tat tca gcc agt tcc atg gca ctg gcc ata gca			1584	
164	Leu Met Met Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala				
165	515	520	525		
167	gca ggt cag agt gtg gtt tct gta gca aca ctt ctc atg acc atc tgt			1632	
168	Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys				
169	530	535	540		
171	ttt gtg ttt atg atg att ttt tca ggt ctg ttg gtc aat ctc aca acc			1680	
172	Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr				
173	545	550	555	560	
175	att gca tct tgg ctg tca tgg ctt cag tac ttc agc att cca cga tat			1728	
176	Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr				
177	565	570	575		
179	gga ttt acg gct ttg cag cat aat gaa ttt ttg gga caa aac ttc tgc			1776	
180	Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys				
181	580	585	590		
183	cca gga ctc aat gca aca gga aac aat cct tgt aac tat gca aca tgt			1824	
184	Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys				
185	595	600	605		
187	act ggc gaa gaa tat ttg gta aag cag ggc atc gat ctc tca ccc tgg			1872	
188	Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp				
189	610	615	620		
191	ggc ttg tgg aag aat cac gtg gcc ttg gct tgt atg att gtt att ttc			1920	
192	Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe				
193	625	630	635	640	

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195 ctc aca att gcc tac ctg aaa ttg tta ttt ctt aaa aaa tat tct taa 1968
 196 Leu Thr Ile Ala Tyr Leu Lys Leu Leu Phe Leu Lys Lys Tyr Ser
 197 645 650 655
 200 <210> SEQ ID NO: 2
 201 <211> LENGTH: 655
 202 <212> TYPE: PRT
 203 <213> ORGANISM: Homo sapiens
 205 <400> SEQUENCE: 2
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 208 1 5 10 15
 211 Thr Asn Gly Phe Pro Ala Thr Ala Ser Asn Asp Leu Lys Ala Phe Thr
 212 20 25 30
 215 Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
 216 35 40 45
 219 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
 220 50 55 60
 223 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
 224 65 70 75 80
 227 Pro Thr Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
 228 85 90 95
 231 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
 232 100 105 110
 235 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Asp Asp
 236 115 120 125
 239 Val Val Met Gly Thr Leu Thr Val Arg Glu Asn Leu Gln Phe Ser Ala
 240 130 135 140
 243 Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
 244 145 150 155 160
 247 Ile Asn Arg Val Ile Gln Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
 248 165 170 175
 251 Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
 252 180 185 190
 255 Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe
 256 195 200 205
 259 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
 260 210 215 220
 263 Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
 264 225 230 235 240
 267 Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
 268 245 250 255
 271 Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
 272 260 265 270
 275 Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
 276 275 280 285
 279 Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
 280 290 295 300
 283 Val Ala Leu Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu
 284 305 310 315 320
 287 Pro Ser Lys Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr

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288 325 330 335
 291 Val Asn Ser Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu
 292 340 345 350
 295 Ser Gly Gly Glu Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser
 296 355 360 365
 299 Tyr Thr Thr Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser
 300 370 375 380
 303 Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile
 304 385 390 395 400
 307 Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu
 308 405 410 415
 311 Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe
 312 420 425 430
 315 Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe
 316 435 440 445
 319 Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr
 320 450 455 460
 323 Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro
 324 465 470 475 480
 327 Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met
 328 485 490 495
 331 Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr
 332 500 505 510
 335 Leu Met Met Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala
 336 515 520 525
 339 Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys
 340 530 535 540
 343 Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr
 344 545 550 555 560
 347 Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr
 348 565 570 575
 351 Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys
 352 580 585 590
 355 Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys
 356 595 600 605
 359 Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp
 360 610 615 620
 363 Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe
 364 625 630 635 640
 367 Leu Thr Ile Ala Tyr Leu Lys Leu Leu Phe Leu Lys Lys Tyr Ser
 368 645 650 655
 371 <210> SEQ ID NO: 3
 372 <211> LENGTH: 18
 373 <212> TYPE: DNA
 374 <213> ORGANISM: Artificial Sequence
 376 <220> FEATURE:
 377 <223> OTHER INFORMATION: Synthetic DNA
 379 <400> SEQUENCE: 3
 380 gtgccccactc aaaagggtt

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